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run on:	April 12, 2005, 10:46:01 ; Search time 167 Seconds (without alignments) 30.107 Million cell updates/sec
title:	US-09-674-616A-2
target score:	67
sequence:	1 NQEQQVSPYLUKG 13
scoring table:	BLOSUM62
gapopen:	10.0 , Gapext: 0.5
searched:	21.05692 seqs, 386760381 residues
number of hits containing chosen parameters:	23870

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minimum DB seq length: 13
maximum DB seq length: 13
minimum DB seq length: 13
maximum DB seq length: 13

post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

database : A_Geneseq_16Dec04;*
  1: _geneseqP1980s;*
  2: _geneseqP1990s;*
  3: _geneseqP2000s;*
  4: _geneseqP2001s;*
  5: _geneseqP2002s;*
  6: _geneseqP2003as;*
  7: _geneseqP2003bs;*
  8: _geneseqP2004s;*

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red. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES						
result	No.	Score	Query	Match	Length	DB
		ID				
A	1	67	100.0	13	3	AYY67835
	2	67	100.0	13	8	ADP44607
	3	64	95.5	13	3	AYY67837
	4	61	91.0	13	3	AYY67836
	5	61	91.0	13	3	AYY67842
	6	59	88.1	13	3	AYY67841
	7	59	88.1	13	3	AYY67840
	8	46	68.7	13	3	AYY67844
	9	36	53.7	13	5	AAM0298
	10	36	53.7	13	6	ABG13917
	11	28	41.8	13	7	ADL4294
	12	27	40.3	13	2	AYY0946
	13	26	38.8	13	2	AYY0420
	14	25	37.3	13	2	AAR4972
	15	25	37.3	13	2	AAW8008
	16	25	37.3	13	5	AAE23145
	17	24	35.8	13	2	AAR4779
	18	24	35.8	13	5	ABJ00698
	19	24	35.8	13	5	ABG5559
	20	24	35.8	13	5	ABB97726
	21	24	35.8	13	5	ABB97727
	22	24	35.8	13	7	ADG14398
	23	24	35.8	13	7	ADG44265
	24	24	35.8	13	7	ADM44811

				Potential
6	35.8	13	7	Adm75341
7	35.8	13	7	Adm75076
8	35.8	13	7	Adm75605
9	35.8	13	7	Adm75390
0	34.3	13	2	Aar9912
1	34.3	13	2	Aar9915
2	34.3	13	2	Aar9913
3	34.3	13	2	Aar0824
4	34.3	13	2	Aar0824
5	34.3	13	2	Aaw06266
6	34.3	13	4	AM53255
7	34.3	13	4	ABB9728
8	34.3	13	6	ADA51575
9	34.3	13	6	ADA51545
0	34.3	13	6	ADA51533
1	34.3	13	6	ADA51556
2	34.3	13	6	ADA51583
3	34.3	13	6	ADA1566
4	34.3	13	7	ADM75719
5	34.3	13	7	ADM74925

ALIGNMENTS

RESULT 1
 AAY67835
 ID AAY67835 standard; peptide; 13 AA.
 XX
 AC AAY67835;
 XX DT 25-APR-2000 (first entry)
 XX DE Alpha-2 antiplasmin enzyme derived peptide #2.
 XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
 KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
 XX

Key	Location/Qualifiers
Modified-site	1 /note= "Asn optionally forms a peptide bond with C-terminal Gly to form a cyclic peptide"
Misc-difference	5 .13 /note= "Optionally D form residues"
Modified-site	13 /note= "Gly optionally forms a peptide bond with N-terminal Asn to form a cyclic peptide"

				Potential
6	35.8	13	7	Adm75341
7	35.8	13	7	Adm75076
8	35.8	13	7	Adm75605
9	35.8	13	7	Adm75390
0	34.3	13	2	Aar9912
1	34.3	13	2	Aar9915
2	34.3	13	2	Aar9913
3	34.3	13	2	Aar0824
4	34.3	13	2	Aar0824
5	34.3	13	2	Aaw06266
6	34.3	13	4	AM53255
7	34.3	13	4	ABB9728
8	34.3	13	6	ADA51575
9	34.3	13	6	ADA51545
0	34.3	13	6	ADA51533
1	34.3	13	6	ADA51556
2	34.3	13	6	ADA51583
3	34.3	13	6	ADA1566
4	34.3	13	7	ADM75719
5	34.3	13	7	ADM74925

ALIGNMENTS

RESULT 1
 AAY67835
 ID AAY67835 standard; peptide; 13 AA.
 XX
 AC AAY67835;
 XX DT 25-APR-2000 (first entry)
 XX DE Alpha-2 antiplasmin enzyme derived peptide #2.
 XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer;
 KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
 XX

Key	Location/Qualifiers
Modified-site	1 /note= "Asn optionally forms a peptide bond with C-terminal Gly to form a cyclic peptide"
Misc-difference	5 .13 /note= "Optionally D form residues"
Modified-site	13 /note= "Gly optionally forms a peptide bond with N-terminal Asn to form a cyclic peptide"

CC detectable moiety can also act as substrates for Factor XIIIa. The
 CC invention relates to compounds which can be used in the diagnosis of
 CC thrombosis or embolism and also for diagnosing atherosclerosis,
 CC inflammation or cancer. The peptide forms part of the compound

XX Sequence 13 AA;

Query Match 100.0%; Score 67; DB 3; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ

Qy 1 NQEQVSPYTLKG 13

Db 1 NQEQVSPYTLKG 13

Query Match 100.0%; Score 67; DB 3; Length 13;

Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 SQ

Qy 1 NQEQVSPYTLKG 13

Db 1 NQEQVSPYTLKG 13

RESULT 2

ADP44607 ADP44607 standard; peptide; 13 AA.

XX AC ADP44607;

XX DT 12-AUG-2004 (First entry)

XX DE Radioisotope technetium-related alpha-antiplasmin mutant peptide 2.

XX KW radioisotope technetium: TC Complex: aza-diaminedioxime ligand;
 KW radiopharmaceutical; thrombus diagnostic imaging; alpha-antiplasmin;
 KW mutant; mutein.

XX OS Synthetic.

XX OS Unidentified.

XX Key Location/Qualifiers

PT /label= OTHER /note= "OTHER = Optionally attached to N-acetyl group"

PT Modified-site 8

PT /label= OTHER /note= "OTHER = Optionally iodoo-Tyr. Substituted wild-type Leu-Thr-Leu"

PT WO2004037297-A1.

XX PN 06-MAY-2004.

XX PD 24-OCT-2003; 2003WO-GB004573.

XX PR 25-OCT-2002; 2002GB-00024799.

XX PA (AMERSHAM PLC.

XX PI Brauers G, Farrar G, Barnett DJ, Wadsworth HJ, Lewis JS;

XX PR 2004-365454/34.

XX PT Composition useful in radiopharmaceuticals for diagnostic imaging of aza-diaminedioxime ligand. The invention relates to a novel composition comprising a complex of a radiopharmaceuticals for diagnostic imaging of aza-diaminedioxime ligand. The composition of the invention may be useful in radiopharmaceuticals for mammalian administration, to be used in diagnostic imaging of thrombi. The composition comprises minimised amounts of lipophilic technetium complex species, thus improving the overall imaging characteristics. The composition does not form a diastereomeric complex as it does not contain a chiral centre and hence does not require purification of the technetium (^{99m}Tc) isomers. The current sequence is that of the radiolotope technetium (^{99m}Tc)-related alpha-antiplasmin mutant biological targeting peptide 2 of the invention.

XX PS Claim 9; Page 7; 50pp; English.

CC The invention relates to a novel composition comprising a complex of a radiopharmaceuticals for diagnostic imaging of aza-diaminedioxime ligand. The composition of the invention may be useful in radiopharmaceuticals for mammalian administration, to be used in diagnostic imaging of thrombi. The composition comprises minimised amounts of lipophilic technetium complex species, thus improving the overall imaging characteristics. The composition does not form a diastereomeric complex as it does not contain a chiral centre and hence does not require purification of the technetium (^{99m}Tc) isomers. The current sequence is that of the radiolotope technetium (^{99m}Tc)-related alpha-antiplasmin mutant biological targeting peptide 2 of the invention.

XX SQ Sequence 13 AA;

Query Match 100.0%; Score 67; DB 8; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.5e-05;
 Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQEQVSPYTLKG 13

Db 1 NQEQVSPYTLKG 13

RESULT 3

AAV67837 AAV67837 standard; peptide; 13 AA.

XX AC AAV67837;

XX DT 25-APR-2000 (First entry)

XX DE Alpha-2 antiplasmin enzyme derived peptide #4.

XX KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis.

XX OS Synthetic.

XX FH Key Location/Qualifiers

PT Modified-site 1 /note= "N-terminal acetyl"

XX FT WO9960018-A1.

XX PN PN 25-NOV-1999.

XX PD 25-NOV-1999.

XX PT 14-MAY-1999;

XX PR 99EP-00303872.

XX PA (AMSH) NYCOMED AMERSHAM PLC.

XX PI Storey AE, Mendizabal M, Champion S, Gibson A, Guillbert B;

XX PI Wilson IA, Knox P;

XX DR WPI; 2000-126380/11.

XX PT Novel synthetic analogues for diagnosis of thrombosis, embolism,

CC atherosclerosis, inflammation or cancer.

XX PS Example 2; Page 16; 46pp; English.

XX PA This sequence represents an alpha-2 antiplasmin derived peptide, Alpha-2

CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor

CC XIIIa. Synthetic analogues of lysine and glutamine labelled with a

CC detectable moiety can also act as substrates for Factor XIIIa. The

CC invention relates to compounds which can be used in the diagnosis of

CC thrombosis or embolism and also for diagnosing atherosclerosis,

CC inflammation or cancer. The peptide forms part of the compound

XX SQ Sequence 13 AA;

Query Match 95.5%; Score 64; DB 3; Length 13;
 Best Local Similarity 92.3%; Pred. No. 5.6e-05;
 Matches 12; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

Qy 1 NQEQVSPYTLKG 13

Db 1 NQQVSPYTLKG 13

RESULT 4

AAV67836 AAV67836 standard; peptide; 13 AA.

ID

XX	AAY67836;	FT	Misc-difference 8	
AC		FT	/note= "D-form residue"	
XX	25-APR-2000 (first entry)	FT	Misc-difference 12	
DT		FT	/note= "D-form residue"	
DE	Alpha-2 antiplasmin enzyme derived peptide #3.	FT	Modified-site 13	
XX		FT	/label= bAla	
KW	Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis.	XX	WO9960018-A1.	
XX		XX	25-NOV-1999.	
OS		XX	14-MAY-1999; 99WO-GB001550.	
XX		XX	15-MAY-1998; 98EP-00303872.	
PH		XX		
FT		XX		
FT		XX		
XX		PA	(AMSH) NYCOMED AMERSHAM PLC.	
PN	W09960018-A1.	XX	Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;	
XX		XX	PI Wilson IA, Knox P;	
XX		XX	DR WPI; 2000-126380/11.	
XX		XX	Novel synthetic analogues for diagnosis of thrombosis, embolism, atherosclerosis, inflammation or cancer.	
XX		XX	Example 2; Page 17; 46pp; English.	
XX		XX	This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2 antiplasmin is a substrate for the fibrin stabilising enzyme Factor XIIIa. Synthetic analogues of lysine and glutamine labelled with a detectable moiety can also act as substrates for Factor XIII. The invention relates to compounds which can be used in the diagnosis of thrombosis or embolism and also for diagnosing atherosclerosis, inflammation or cancer. The peptide forms part of the compound	
XX		XX	Sequence 13 AA;	
PS	Example 2; Page 16; 46pp; English.	PS	Query Match 91.0%; Score 61; DB 3; Length 13;	
XX		XX	Best Local Similarity 100.0%; Pred. No. 0 00021;	
CC	This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2 antiplasmin is a substrate for the fibrin stabilising enzyme Factor XIIIa. Synthetic analogues of lysine and glutamine labelled with a detectable moiety can also act as substrates for Factor XIII. The invention relates to compounds which can be used in the diagnosis of thrombosis or embolism and also for diagnosing atherosclerosis, inflammation or cancer. The peptide forms part of the compound	CC	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		XX	Qy 1 NQEQQVSPYTLK 12	
XX		XX	Db 1 NQEQQVSPYTLK 12	
PS	Example 2; Page 16; 46pp; English.	PS	RESULT 6	
XX		XX	Query Match 91.0%; Score 61; DB 3; Length 13;	
CC	This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2 antiplasmin is a substrate for the fibrin stabilising enzyme Factor XIIIa. Synthetic analogues of lysine and glutamine labelled with a detectable moiety can also act as substrates for Factor XIII. The invention relates to compounds which can be used in the diagnosis of thrombosis or embolism and also for diagnosing atherosclerosis, inflammation or cancer. The peptide forms part of the compound	CC	Best Local Similarity 100.0%; Pred. No. 0 00021;	
XX		XX	Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;	
XX		XX	Qy 1 NQEQQVSPYTLK 12	
XX		XX	Db 1 NQEQQVSPYTLK 12	
PS	Example 2; Page 16; 46pp; English.	PS	Alpha-2 antiplasmin enzyme derived peptide #8.	
XX		XX	KW Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIa; cancer; embolism; thrombosis; inflammation; atherosclerosis; diagnosis.	
XX		XX	OS Synthetic.	
XX		XX	FT Location/Qualifiers	
XX		XX	FT 1	
XX		XX	FT /note= "N-terminal acetyl"	
XX		XX	FT 8	
XX		XX	FT /note= "2-Naphthylalanine"	
XX		XX	PN W09960018-A1.	
OS		XX	25-NOV-1999.	
XX		XX	PD WPI; 14-MAY-1999; 99WO-GB001550.	
PH		XX		
FT		XX		
FT		XX		
XX		XX		
Key	Location/Qualifiers			
Modified-site	1			
	/note= "N-terminal acetyl"			

PR 15-MAY-1998; 98EP-00303872.
 XX (AMSH) NYCOMED AMERSHAM PLC.
 PA Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
 PI Wilson IA, Knox P;
 XX WPI; 2000-126380/11.
 XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
 PT atherosclerosis, inflammation or cancer.
 XX Example 2; Page 16; 46pp; English.
 XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
 CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
 XIIIA. Synthetic analogues of lysine and glutamine labelled with a
 detectable moiety can also act as substrates for Factor XIIIA. The
 invention relates to compounds which can be used in the diagnosis of
 CC thrombosis or embolism and also for diagnosing atherosclerosis,
 CC inflammation or cancer. The peptide forms part of the compound
 CC XX Sequence 13 AA;
 SQ

Query Match 88.1%; Score 59; DB 3; Length 13;
 Best Local Similarity 92.3%; Pred. No. 0.00049;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NQEQVSPYTLKG 13
 Db 1 NQEQVSPYTLKG 13

RESULT 8
 AAY67844
 ID AAY67844 standard; peptide; 13 AA.
 AC AAY67844;
 XX DT 25-APR-2000 (first entry)
 AC AAY67844;
 XX DE Alpha-2 antiplasmin enzyme derived peptide #11.
 XX Alpha-2 antiplasmin; fibrin stabilising enzyme; Factor XIIIA; cancer;
 KW embolism; thrombosis; inflammation; atherosclerosis; diagnosis.
 KW Synthetic.
 XX OS
 XX PN WO960018-A1.
 XX PD 25-NOV-1999.
 XX PF 14-MAY-1999;
 XX PR 15-MAY-1998;
 XX PA (AMSH) NYCOMED AMERSHAM PLC.
 XX PI Storey AE, Mendizabal M, Champion S, Gibson A, Guilbert B;
 XX PI Wilson IA, Knox P;
 XX DR 98EP-00303872.
 XX WPI; 2000-126380/11.
 XX PT Novel synthetic analogues for diagnosis of thrombosis, embolism,
 PT atherosclerosis, inflammation or cancer.
 XX PS Example 2; Page 17; 46pp; English.
 XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2
 CC antiplasmin is a substrate for the fibrin stabilising enzyme Factor
 XIIIA. Synthetic analogues of lysine and glutamine labelled with a
 detectable moiety can also act as substrates for Factor XIIIA. The
 invention relates to compounds which can be used in the diagnosis of
 CC thrombosis or embolism and also for diagnosing atherosclerosis,
 CC inflammation or cancer. The peptide forms part of the compound
 CC XX Sequence 13 AA;
 SQ

Query Match 68.7%; Score 46; DB 3; Length 13;
 Best Local Similarity 69.2%; Pred. No. 0.14;
 Matches 9; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

Qy 1 NQEQVSPYTLKG 13
 Db 1 NQEQVSPYAAAG 13

RESULT 9
 XX Novel synthetic analogues for diagnosis of thrombosis, embolism,
 XX atherosclerosis, inflammation or cancer.
 XX PS Example 2; Page 16; 46pp; English.
 XX This sequence represents an alpha-2 antiplasmin derived peptide. Alpha-2

used of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated proteins Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofibrillary acidic protein (GFAP), presenilin I, presenilin II, glial fibrillary acidic protein (GFP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A

SQ Sequence 13 AA;

Query Match 40.3%; Score 27; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 4; Nismatches 1; Indels 0;

Qy 2 QEQQVSYTL 10

Db 4 RREMSPYSL 12

RESULT 13

AYA20420 ID AAY20420 standard; protein; 13 AA.
XX

AC AAY20420;

XX DT 22-JUL-1999 (First entry)

Human microtubule associated protein 2 mutant fragment 116.
DE Human microtubule associated protein 2 mutant fragment 116.
XX Human; beta-amyloid precursor protein; beta-APP; diagnosis; cancer;
KW frameshift; mutation; age-related disease; neurodegenerative disorder;
KW Alzheimer's disease; Down's syndrome; myotonic dystrophy; neuronal;
KW Huntington's disease; multiple sclerosis; alcoholic liver disease;
KW diabetes mellitus type II; microtubule associated protein; Tau; Big Tau;
KW ubiquitin B; apolipoprotein E; MAP2; neurofilament-L; neurofibrillary acidic protein; presenilin I; presenilin II; cellular tumour antigen;
KW glial fibrillary acidic protein; GFP; p53; semaphorin III; HUPF-1;
KW bcl-2; B-cell leukemia/lymphoma 2 proto-oncogene; HMGP-C; NSP-A;
KW high mobility group protein-C; neuroendocrine specific protein A.

OS Synthetic.

OS Homo sapiens.

XX PN W09845322-A2.

XX PD 15-OCT-1998.

XX PF 02-APR-1998; 98W0-1B000705.

XX PR 10-APR-1997; 97US-0043163P.

XX PA (ROYA-) ROYAL NETHERLANDS ACADEMIA SCI.

PA (UYRO-) UNIV ROTTERDAM ERASMUS.

PA (UYOT-) RIJKSUNIV Utrecht.

XX PI Van Leeuwen FW, Grosveid FG, Burbach JPH;

XX DR WPI: 1998-609901/51.

DR N-PSDB; AAX7557.

Diagnosing disease by detecting frameshift mutations in RNA or corresponding protein mutations - used to diagnose cancer and neurological diseases, particularly Alzheimer's disease, and also for treatment and prevention with specific ribozymes or wild-type RNA.

XX Disclosure; Fig 6; 258pp; English.

This invention describes a novel method for the diagnosis of a disease caused by, or associated with, an RNA molecule that has a frameshift mutation. The method is used to diagnose age-related diseases, especially cancer and a wide range of neurodegenerative disorders (e.g., Alzheimer's disease, Down's syndrome, myotonic dystrophy, Huntington's disease,

multiple sclerosis, alcoholic liver disease, diabetes mellitus type II and many others listed) or susceptibility to these disorders. The method allows a definitive diagnosis of Alzheimer's disease in living patients, at an early stage. It is based on the observation that disease may be caused by mutations in RNA rather than DNA. The invention describes the use of neuronal system RNA molecules, specifically proteins including beta-amyloid precursor protein (beta-APP), the microtubule associated protein Tau and Big Tau, ubiquitin B, apolipoprotein E, microtubule associated protein 2 (MAP2), neurofilament-L, neurofilament-M, neurofilament-F, presenilin I, presenilin II, glial fibrillary acidic protein (GFAP), the cellular tumour antigen p53, B-cell leukemia/lymphoma 2 (bcl-2) proto-oncogene, semaphorin III, HUPF-1, high mobility group protein-C (HMGP-C) and neuroendocrine specific protein A

SQ Sequence 13 AA;
Query Match 40.3%; Score 27; DB 2; Length 13;
Best Local Similarity 44.4%; Pred. No. 5.4e+02;
Matches 4; Conservative 4; Nismatches 1; Indels 0;

Qy 2 QEQQVSYTL 10

Db 4 RREMSPYSL 12

RESULT 14

AAR54972

ID AAR54972 standard; peptide; 13 AA.

XX DE AAR54972;
XX AC AAR54972;
XX DT 25-MAR-2003 (revised)
KW 31-OCT-1994. (First entry)
XX Sothi grass pollen allergen T cell epitope.
XX IgE; allergy; antigen; diagnosis; treatment; Group I allergen.
XX KW Sorghum halepense.
XX OS W09410314-A1.
XX PN W09410314-A1.
XX PD 11-MAY-1994.
XX PF 29-OCT-1993; 93W0-AU000559.
XX PR 30-OCT-1992; 92US-00971096.
XX PA (UTMB) UNIV MELBOURNE.
XX PI Singh MB, Knox RB, Avijoglu A;
XX WPI: 1994-167469/20.
XX PT DNA encoding allergenic proteins and peptide(s) From Johnson grass pollen allergen Sothi - for diagnosing, treating and preventing allergy to Johnson pollen.
XX SQ Sequence 13 AA;

XX PS Claim 20; Fig 9; 81pp; English.

XX The sequence is that of a Sothi Group I grass pollen allergen T cell epitope corresp. to residues 93-105 of Sothi clone 3S. See also AAR54949-76. (Updated on 25-MAR-2003 to correct PN field.)
XX SQ Query Match 37.3%; Score 25; DB 2; Length 13;
Best Local Similarity 50.0%; Pred. No. 1.3e+03;
Matches 4; Conservative 2; Nismatches 2; Indels 0;
Gaps 0;

Qy 1 NOEQVSPY 8
Db 4 NYEQIAY 11

Search completed: April 12, 2005, 10:48:58
 Job time : 169 secs

RESULT 15
 AAW38008 standard; peptide; 13 AA.
 ID AAW38008
 XX
 AC AAW38008;
 XX
 DT 23-APR-1998 (first entry)

XX WW domain binding clone 4 obtained from a pp library.
 DE
 KW Peptide recognition unit; WW domain; cell signalling; growth regulation;
 KW cytoskeleton organisation; targeted drug screening; modulator;
 KW WW domain interaction.
 XX

OS Synthetic.

XX Key Location/Qualifiers
 PH 6..9
 FT /note= "PPPPV motif"
 XX W09737223-A1.

XX PD 09-OCT-1997.

XX PF 03-APR-1997; 9700-US005547.

XX PR 03-APR-1996; 96US-00630916.

XX PA (CYTO-) CYTOGEN CORP.

PA (UYNC-) UNIV NORTH CAROLINA.

XX PI Pirozzi G, Kay BK, Fowlkes DM;

XX DR 1997-503234/46.

XX Identifying cell signalling and growth regulatory polypeptides by
 PT reaction with multivalent recognition complex - Polypeptides are useful
 PT in targeted drug selection.
 XX

PS Claim 92; Fig 27; 220pp; English.

XX Peptides AAW38005-08 are the sequences of WW domain binding clones
 CC obtained by screening random or biased libraries with the WW domains of
 CC the novel WWP proteins. The present peptide was obtained after screening
 CC with WW domain 1 of WWP1 (WWP1.1). The peptides are peptide recognition
 CC units ("ligands"), and are used for analysing specificities of the WW
 CC domains. The WW domain is a small functional domain. Its name is derived
 CC from the observation that two tryptophan residues, one in the amino
 CC terminal portion of the WW domain and one in the carboxyl terminal
 CC portion, are conserved. Most proteins containing WW domains have a
 CC function involving cell signalling and growth regulation or the
 CC organisation of the cytoskeleton. Polypeptides containing a WW domain are
 CC identified by treating a multivalent recognition unit complex that has
 CC selective binding affinity for a WW domain, with many polypeptides and
 CC identifying those with selective affinity for the complex. Proteins
 CC containing WW domains are used for targeted drug screening, i.e. to
 CC identify potential modulators of specific WW domain interactions. note:
 CC sequence in SEQ ID listing differs from sequence given in Figure. The SEQ
 CC ID sequence is as follows: GPSBOPPPYETVK

XX Sequence 13 AA;

SQ Query Match Score 25; DB 2; Length 13;
 Best Local Simillarity 37.3%; Pred. No. 1.3e+03;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;
 Qy 3 EQVSPYTLK 12
 Db 4 EQPBPYETVK 13

STREET: 1100 NEW YORK AVENUE, N.W.
 CITY: WASHINGTON
 STATE: D.C.
 COUNTRY: USA
 ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/174,467
 FILING DATE: 28-DEC-1993
 CLASSIFICATION: 800
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/874,166
 FILING DATE: 27-APR-1992
 ATTORNEY/AGENT INFORMATION:
 NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 95563/PS36321/US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 13 amino acids
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-174-467-6

Query Match 35.8%; Score 24; DB 1; Length 13;
 Best Local Similarity 80.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;
 Qy 5 VSPYT 9
 Db 5 LSPYT 9

RESULT 3
 US-08-452-071-6

; Sequence 6, Application US/08452071
 ; Parent No. 6066780
 ; GENERAL INFORMATION:
 ; APPLICANT: BOUDET, ALAIN M.
 ; APPLICANT: INZE, DIRK G.
 ; APPLICANT: SCHUCH, WOLFGANG W.
 ; TITLE OF INVENTION: MODIFICATION OF LIGNIN SYNTHESIS IN
 ; TITLE OF INVENTION: PLANTS
 ; NUMBER OF SEQUENCES: 23
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: CUSHMAN, DARBY & CUSHMAN
 ; STREET: 1100 NEW YORK AVENUE, N.W.
 ; CITY: WASHINGTON
 ; STATE: D.C.
 ; ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/452,071
 FILING DATE:
 CLASSIFICATION:
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: US 07/874,166
 FILING DATE: 27-APR-1992
 ATTORNEY/AGENT INFORMATION:

NAME: KOKULIS, PAUL N.
 REGISTRATION NUMBER: 16,773
 REFERENCE/DOCKET NUMBER: 95563/PS36321/US
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 202-861-3000
 TELEFAX: 202-822-0944
 INFORMATION FOR SEQ ID NO: 6:
 LENGTH: 13 amino acids
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: amino acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: peptide
 US-08-452-071-6

Query Match 35.8%; Score 24; DB 3; Length 13;
 Best Local Similarity 90.0%; Pred. No. 3.8e+02;
 Matches 4; Conservative 1; Mismatches 0; Gaps 0;
 Qy 5 VSPYT 9
 Db 5 LSPYT 9

RESULT 4
 US-08-620-213-3

; Sequence 3, Application US/08620213
 ; Patent No. 5677297
 ; GENERAL INFORMATION:
 ; APPLICANT: WALDICK, Harald
 ; APPLICANT: HOELTJE, Dagmar
 ; APPLICANT: MESSINGER, Josef
 ; APPLICANT: ANTEL, Jochen
 ; APPLICANT: WURL, Michael
 ; APPLICANT: THORNWAHLIN, Dirk
 ; TITLE OF INVENTION: BENZAZEPINE- AND BENZOAZEPINE- AND BENZOTIAZEPINE-N-ACETIC ACID DERIVATIVES, PROCESS FOR THEIR PREPARATION AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM

; NUMBER OF SEQUENCES: 3
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Eversion, McKeown, Edwards & Lenahan
 ; STREET: 1200 G Street, N.W., Suite 700
 ; CITY: Washington
 ; STATE: DC
 ; COUNTRY: USA
 ; ZIP: 20005
 COMPUTER READABLE FORM:
 MEDIUM TYPE: floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/620,213
 FILING DATE:
 CLASSIFICATION: 544
 PRIOR APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: EVANS, Joseph D.
 ; REGISTRATION NUMBER: 26,269
 ; REFERENCE/DOCKET NUMBER: 181/42626
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (202) 628-8800
 ; TELEFAX: (202) 628-8844
 ; INFORMATION FOR SEQ ID NO: 3:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-620-213-3

Query Match 34.3%; Score 23; DB 1; Length 13;
 Best Local Similarity 62.5%; Pred. No. 6e+02;
 Matches 5; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 10
 Db 5 EHVVYGL 12

RESULT 5

US-08-542-686-1

; Sequence 1, Application US/085442686

; GENERAL INFORMATION:

; APPLICANT: Ravetch, Jeffrey V.

; APPLICANT: Kuroski, Tomohiro

; TITLE OF INVENTION: METHOD FOR SCREENING FOR TARGETS FOR

; TITLE OF INVENTION: ANTI-INFLAMMATORY OR ANTI-ALLERGIC AGENTS

; NUMBER OF SEQUENCES: 9

; CURRENT APPLICATION DATA:

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Cooper & Dunham

; STREET: 30 Rockefeller Plaza

; CITY: New York

; STATE: New York

; COUNTRY: USA

; ZIP: 10112

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/542,686

; FILING DATE:

; CLASSIFICATION: 514

; PRIORITY APPLICATION NUMBER: US 08/052,269

; FILING DATE: 23-APR-1993

; ATTORNEY/AGENT INFORMATION:

; NAME: White, John J.

; REGISTRATION NUMBER: 28,678

; REFERENCE/DOCKET NUMBER: 42113/JPW/ARC

; TELEPHONE: (212) 977-9550

; INFORMATION FOR SEQ ID NO: 1:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-542-686-1

Query Match 34.3%; Score 23; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 12
 Db 2 ENTITYSLLK 11

RESULT 6

US-08-332-562A-69

; Sequence 69, Application US/08332562A

; GENERAL INFORMATION:

; APPLICANT: MCKENZIE, Ian F.C.

; APPLICANT: HOGARTH, Mark P.

; APPLICANT: HIBBS, Margaret L.

; APPLICANT: SCOTT, Bernadette M.

; APPLICANT: BONADONNA, Lisa D.

; APPLICANT: HULETT, Mark D.

; TITLE OF INVENTION: PC RECEPTOR FOR IMMUNOGLOBULIN

; NUMBER OF SEQUENCES: 136

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.3.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/332,562A

; FILING DATE: 31-OCT-1994

; CLASSIFICATION: 435

; PRIORITY APPLICATION NUMBER: US 07/896,457

; APPLICATION NUMBER: US/08/332,562A

; FILING DATE: 27-MAY-1992

; ATTORNEY/AGENT INFORMATION:

; NAME: BENT, Stephen A.

; REGISTRATION NUMBER: 29,768

; REFERENCE/DOCKET NUMBER: 54270/119/GRHA

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399

; TELEX: 904136

; INFORMATION FOR SEQ ID NO: 69:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 13 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; US-08-332-562A-69

Query Match 34.3%; Score 23; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 6e+02;
 Matches 5; Conservative 1; Mismatches 4; Indels 0; Gaps 0;

Qy 3 EQVSPYTLK 12
 Db 1 ENTITYSLLK 10

RESULT 7

US-08-058-947-14

; Sequence 14, Application US/08068947

; GENERAL INFORMATION:

; APPLICANT: Sepetov, Nikolai

; APPLICANT: Lissakova, Olga

; APPLICANT: Krchnak, Viktor

; APPLICANT: Lebl, Michal

; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS SPECTROMETRY

; NUMBER OF SEQUENCES: 47

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Pennie & Edmonds

; STREET: 1155 Avenue of the Americas

; STATE: New York

; COUNTRY: USA

; ZIP: 10036

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; ;

OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent In Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/068,947
 FILING DATE: 19930528
 CLASSIFICATION: 436
 ATTORNEY/AGENT INFORMATION:
 NAME: Misrock, Esq., S. Leslie
 REGISTRATION NUMBER: 18,872
 REFERENCE/DOCKET NUMBER: 7156-040-999
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 212-790-9090
 TELEFAX: 212-866-8864/9741
 TELEX: 66141 PENNIE
 US-08-68-947-14
 SEQUENCE CHARACTERISTICS:
 LENGTH: 13 amino acids
 TYPE: AMINO ACID
 STRANDEDNESS: unknown
 TOPOLOGY: unknown
 MOLECULE TYPE: peptide
 US-08-68-947-14

Query Match 32.8%; Score 22; DB 1; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 2 EQVSP 7
 Db 2 QDQIQP 7

RESULT 9
 US-08-750-419A-22
 Sequence 22, Application US/08750419A
 ; Patent No. 600340
 ; GENERAL INFORMATION:
 ; APPLICANT: BALI, TANJA
 ; APPLICANT: VRTALA, SUSANNE
 ; APPLICANT: SPERR, WOLFGANG
 ; APPLICANT: SIEBEL, CHRISTIAN
 ; APPLICANT: KRAFT, DIETRICH
 ; APPLICANT: LAFFER, SYLVIA
 ; APPLICANT: LAFER, SYLVIA
 ; APPLICANT: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF,
 ; VECTORS AND HOSTS
 ; TITLE OF INVENTION: RECOMBINANT RECOMBINANT DNA MOLECULES,
 ; VECTORS AND HOSTS
 ; TITLE OF INVENTION: CORRESPONDING RECOMBINANT DNA MOLECULES,
 ; VECTORS AND HOSTS
 ; TITLE OF INVENTION: CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC
 ; NUMBER OF SEQUENCES: 33
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: BIRCH, STEWART, KOLASCH AND BIRCH
 ; STREET: PO BOX 747
 ; CITY: FALLS CHURCH
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22040-0747
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: FLOPPY disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent In Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/750,419A
 ; FILING DATE:
 ; CLASSIFICATION: 536
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: MURPHY, JR., GERALD M.
 ; REGISTRATION NUMBER: 28,977
 ; REFERENCE/DOCKET NUMBER: 1614-175
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 205-8000
 ; TELEFAX: (703) 205-8050
 ; INFORMATION FOR SEQ ID NO: 22:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: not relevant
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: peptide
 US-08-750-419A-22

Query Match 32.8%; Score 22; DB 3; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;

Qy 3 EQVSP 8
 Db 1 EPIAPP 6

RESULT 10
 US-09-468-578-11

Sequence 11: Application US/09468578
 ; Patent No. 6399329
 ; GENERAL INFORMATION:
 ; APPLICANT: Wang, Huaming
 ; BODIE, Elizabeth A.
 ; TITLE OF INVENTION: Phenol Oxidizing Enzymes
 ; CURRENT APPLICATION NUMBER: US/09/468,578
 ; CURRENT FILING DATE: 1999-12-21
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/220,871
 ; PRIOR FILING DATE: 1999-06-23
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 11
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Stachybotrys chartarum
 US-09-674-616a-2

Query Match 32.8%; Score 22; DB 3; Length 13;
 Best Local Similarity 80.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Query 4 QVSPY 8
 Db 3 QVMPY 7

RESULT 11
 US-09-674-616a-2
 ; Sequence 11: Application US/09468578
 ; Patent No. 6399329
 ; GENERAL INFORMATION:
 ; APPLICANT: UNILEVER N.V. et al.
 ; TITLE OF INVENTION: DETERGENT COMPOSITIONS COMPRISING PHENOL OXIDIZING ENZYMES
 ; FILE REFERENCE: 7516 (V)
 ; CURRENT APPLICATION NUMBER: US/09/468,819
 ; CURRENT FILING DATE: 2001-06-12
 ; PRIOR FILING DATE: 1998-12-23
 ; PRIOR APPLICATION NUMBER: US 09/338,723
 ; PRIOR FILING DATE: 1999-06-23
 ; NUMBER OF SEQ ID NOS: 17
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO: 11
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Stachybotrys chartarum
 US-09-674-616a-2

Query Match 32.8%; Score 22; DB 4; Length 13;
 Best Local Similarity 80.0%; Pred. No. 9.3e+02;
 Matches 4; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
 Query 4 QVSPY 8
 Db 3 QVMPY 7

RESULT 12
 US-09-674-616a-2
 ; Sequence 12: Application US/09468578
 ; Patent No. 6399329
 ; GENERAL INFORMATION:
 ; APPLICANT: BALT, Tanja
 ; APPLICANT: VRTALA, Susanne
 ; APPLICANT: SPEER, Wolfgang
 ; APPLICANT: VALENT, Peter
 ; APPLICANT: SUSANI, Markus
 ; APPLICANT: KRAFT, Dietrich

; APPLICANT: VALENTA, Rudolf
 ; APPLICANT: LAFER, Sylvia
 ; TITLE OF INVENTION: RECOMBINANT ALLERGEN, FRAGMENTS THEREOF, CORRESPONDING RECOMBINANT MOLECULES, VECTORS AND HOSTS CONTAINING THE DNA MOLECULES, DIAGNOSTIC AND THERAPEUTIC USES OF SAID ALLERGENS AND FRAGMENTS
 ; FILE REFERENCE: 1614-0247P
 ; CURRENT APPLICATION NUMBER: US/09/611,672
 ; CURRENT FILING DATE: 2001-03-20
 ; NUMBER OF SEQ ID NOS: 28
 ; SOFTWARE: PatentIn version 3.1
 ; SEQ ID NO: 19
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Timothy Grass
 US-09-674-616a-2

Query Match 32.8%; Score 22; DB 4; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9.3e+02;
 Matches 3; Conservative 2; Mismatches 1; Indels 0; Gaps 0;
 Query 3 EQVSPY 8
 Db 1.EPIATPY 6

RESULT 13
 US-09-674-616a-2
 ; Sequence 13: Application US/09468578
 ; Patent No. 5470753
 ; GENERAL INFORMATION:
 ; APPLICANT: Sepetov, Nikolai
 ; APPLICANT: Lissakova, Olga
 ; APPLICANT: Krchhak, Viktor
 ; APPLICANT: Lebl, Michal
 ; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS SPECTROMETRY
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/068,947
 ; FILING DATE: 19930528
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mistock Esq., S. Leslie
 ; REGISTRATION NUMBER: 18,872
 ; REFERENCE/DOCKET NUMBER: 7156-040-999
 ; TELEPHONE: 212-869-9090
 ; TELEFAX: 212-869-8844/9741
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 19:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 13 amino acids
 ; TYPE: AMINO ACID
 ; STRANDEDNESS: unknown
 ; TOPOLOGY: unknown
 ; MOLECULE TYPE: peptide
 US-09-674-616a-2

Query Match 31.3%; Score 21; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.5e+03;
 Matches 3; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

RESULT 14
 US-09-040-216-8
 ; Sequence 8, Application US/09040216
 ; Patent No. 6030942
 ; GENERAL INFORMATION:
 ; APPLICANT: COOPERMAN, ET AL., BARRY
 ; TITLE OF INVENTION: PEPTIDES, PEPTIDE ANALOGS, PEPTIDOMIMETICS, AND OTHER
 ; SMALL MOLECULES USEFUL FOR INHIBITING THE ACTIVITY OF
 ; RIBONUCLEOTIDE REDUCTASE
 ; FILE REFERENCE: 9596-63U1
 ; CURRENT APPLICATION NUMBER: US/09/040,216
 ; CURRENT FILING DATE: 1998-03-17
 ; EARLIER APPLICATION NUMBER: 08,919,748
 ; EARLIER FILING DATE: 1997-08-28
 ; EARLIER APPLICATION NUMBER: 60,025,146
 ; EARLIER FILING DATE: 1996-08-30
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 8
 ; LENGTH: 13
 ; TYPE: PRT
 ; ORGANISM: Escherichia coli
 ; FEATURE:
 ; OTHER INFORMATION: alpha 13 helix region of E. coli R1
 US-09-040-216-8

Query Match 30.6%; Score 20.5%; DB 3; Length 13;
 Best Local Similarity 85.%; Pred. No. 1.8e+03;
 Matches 6; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 8 YT-LIKG 13
 Db 5 YTRILKG 11

RESULT 15
 US-09-068-947-21
 ; Sequence 21, Application US/08068947
 ; Patent No. 5,70753
 ; GENERAL INFORMATION:
 ; APPLICANT: Septov, Nikolai
 ; APPLICANT: Liseakova, Olga
 ; APPLICANT: Krchnak, Viktor
 ; APPLICANT: Lebl, Michal
 ; TITLE OF INVENTION: PEPTIDE SEQUENCING USING MASS
 ; TITLE OF INVENTION: SPECTROMETRY
 ; NUMBER OF SEQUENCES: 47
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: PatentIn Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/068,947
 ; FILING DATE: 19930528
 ; CLASSIFICATION: 436
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Mirock Esq., S. Leslie
 ; REGISTRATION NUMBER: 10,872
 ; REFERENCE/DOCKET NUMBER: 7156-040-999

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OM protein - protein search, using sw model

Run on: April 12, 2005, 10:49:51 ; Search time 129 Seconds (without alignments)

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Title: US-09-674-616A-2

Perfect score: 67

Sequence: 1 NQEQQSPYTLKG 13

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Searched: 1418010 seqs, 331997259 residues

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Minimum DB seq length: 13

Maximum DB seq length: 13

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing First 45 summaries

Database : Published Applications AA:^{*}

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3: /cgn2_6/podata/1/pubpa/us05_pubcomb.pep:*

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19: /cgn2_6/podata/1/pubpa/us50_new_pub.pep:*

20: /cgn2_6/podata/1/pubpa/us60_pubcomb.pep:*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	DB ID	Description
1	36	53.7	13	14	US-10-323-046-22	Sequence 22, App1
2	24	35.8	13	10	US-09-932-613-156	Sequence 156, App
3	24	35.8	13	10	US-09-932-322-156	Sequence 155, App
4	24	35.8	13	15	US-10-361-208-64	Sequence 64, App
5	24	35.8	13	15	US-10-361-208-197	Sequence 197, App
6	24	35.8	13	17	US-10-851-637-87	Sequence 87, App
7	24	35.8	13	17	US-10-851-637-88	Sequence 88, App
8	23	34.3	13	14	US-10-226-007-782	Sequence 782, App
9	23	34.3	13	14	US-10-226-007-794	Sequence 794, App
10	23	34.3	13	14	US-10-226-007-805	Sequence 805, App
11	23	34.3	13	14	US-10-226-007-815	Sequence 815, App
12	23	34.3	13	14	US-10-226-007-824	Sequence 824, App
13	23	34.3	13	14	US-10-226-007-832	Sequence 832, App

Query Match 53.7%; Score 36; DB 14; Length 13;
Best Local Similarity 100.0%; Pred. No. 8 ;
Matches 7; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;

Query Match 1 NQEQQSP 7
2 NQEQQSP 8

RESULT 2

US-09-932-613-156

Sequence 156, Application US/0932613

Publication No. US2003009156A1

GENERAL INFORMATION:

APPLICANT: Human Genome Sciences, Inc.

APPLICANT: Belitzer, James P.

APPLICANT: Potter, M. Daniel

APPLICANT: Fleming, Tony J.

APPLICANT: Rosen, Craig A.

TITLE OF INVENTION: BINDING POLYPEPTIDES AND METHODS BASED THEREON

FILE REFERENCE: DDX-025.1 PCT; DDX-025.1 US

CURRENT APPLICATION NUMBER: US/09/332,613

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: PatentIn version 3.1

SEQ ID NO 156

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Blys binding polypeptide

US-09-932-613-156

Query Match 35.8%; Score 24; DB 10; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.5e+03;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 QVSPYTLK 12

Db 2 QVDPETGLK 10

RESULT 3

US-09-932-322-156

Sequence 156, Application US/0932322

Publication No. US2003019473A1

GENERAL INFORMATION:

APPLICANT: Dyax Corp.

APPLICANT: Belitzer, James P.

APPLICANT: Potter, M. Daniel

APPLICANT: Fleming, Tony J.

APPLICANT: Ladner, Robert Charles

TITLE OF INVENTION: BINDING POLYPEPTIDES FOR B LYMPHOCYTE STIMULATOR PROTEIN (BLYSP)

FILE REFERENCE: DDX-018.1 PCT; DDX-018.1 US

CURRENT APPLICATION NUMBER: US/09/932,322

CURRENT FILING DATE: 2001-08-17

NUMBER OF SEQ ID NOS: 458

SOFTWARE: PatentIn version 3.1

SEQ ID NO 156

LENGTH: 13

TYPE: PRT

ORGANISM: Artificial Sequence

FEATURE: OTHER INFORMATION: Blys binding polypeptide

US-09-932-322-156

Query Match 35.8%; Score 24; DB 10; Length 13;

Best Local Similarity 66.7%; Pred. No. 1.5e+03;

Matches 6; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 4 QVSPYTLK 12

Db 2 QVDPETGLK 10

RESULT 4

US-10-361-008-64

Sequence 64, Application US/10361208

Publication No. US2004000916A1

GENERAL INFORMATION:

APPLICANT: Rider, Todd H.

APPLICANT: Belitzer, James P.

APPLICANT: Potter, M. Daniel

APPLICANT: Fleming, Tony J.

APPLICANT: Ladner, Robert Charles

TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS

FILE REFERENCE: 0050-2041-003

CURRENT APPLICATION NUMBER: US/10/361,208

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: US 60/355,359

PRIOR FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: US 60/355,022

PRIOR FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: US 60/432,386

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 473

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 64

LENGTH: 13

TYPE: PRT

ORGANISM: unknown

FEATURE: OTHER INFORMATION: partial Hdj-1 sequence

FEATURE: NAME/KEY: NON_CONS

LOCATION: 7-8

US-10-361-208-64

Query Match 35.8%; Score 24; DB 15; Length 13;

Best Local Similarity 83.3%; Pred. No. 1.5e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QEQVSP 7

Db 7 QEQQVLP 12

RESULT 5

US-10-361-208-197

Sequence 197, Application US/10361208

Publication No. US2004000916A1

GENERAL INFORMATION:

APPLICANT: Rider, Todd H.

APPLICANT: Belitzer, James P.

APPLICANT: Potter, M. Daniel

APPLICANT: Fleming, Tony J.

APPLICANT: Ladner, Robert Charles

TITLE OF INVENTION: ANTI-PATHOGEN TREATMENTS

FILE REFERENCE: 0050-2041-003

CURRENT APPLICATION NUMBER: US/10/361,208

CURRENT FILING DATE: 2003-02-07

PRIOR APPLICATION NUMBER: US 60/355,359

PRIOR FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: US 60/355,022

PRIOR FILING DATE: 2002-02-07

PRIOR APPLICATION NUMBER: US 60/432,386

PRIOR FILING DATE: 2002-12-10

NUMBER OF SEQ ID NOS: 473

SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 197

LENGTH: 13

TYPE: PRT

ORGANISM: unknown

FEATURE: OTHER INFORMATION: partial Hdj-1 sequence

FEATURE: NAME/KEY: NON_CONS

LOCATION: 7-8

US-10-361-208-197

Query Match 35.8%; Score 24; DB 15; Length 13;

Best Local Similarity 83.3%; Pred. No. 1.5e+03;

Matches 5; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 2 QEQVSP 7

Db 7 QEQQVLP 12

RESULT 6

US-10-851-637-87

Sequence 87, Application US/10851637
 Publication No. US20050015039A1
 GENERAL INFORMATION:
 APPLICANT: Salzwedel, Karl
 APPLICANT: Li, Feng
 APPLICANT: Wild, Carl T.
 APPLICANT: Allaway, Graham P.
 APPLICANT: Freed, Eric O.
 TITLE OF INVENTION: Inhibition of HIV-1 Replication by Distribution of the Processing
 of the Viral Capsid-Spacer Peptide 1 Protein
 FILE REFERENCE: 1900_0430003
 CURRENT APPLICATION NUMBER: US/10/851,637
 CURRENT FILING DATE: 2004-05-24
 PRIOR APPLICATION NUMBER: US 10/766,528
 PRIOR FILING DATE: 2004-01-29
 PRIOR APPLICATION NUMBER: US 60/496,660
 PRIOR FILING DATE: 2003-08-21
 PRIOR APPLICATION NUMBER: US 60/443,180
 PRIOR FILING DATE: 2004-01-29
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 87
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Mutant SP1 region in HIV-1 NL4-3
 US-10-851-637-87

Query Match 35.8%; Score 24; DB 17; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPYTL 11
 Db 6 QVNPATIM 13

RESULT 7
 US-10-851-637-88
 Sequence 88, Application US/10851637
 Publication No. US20050015039A1
 GENERAL INFORMATION:
 APPLICANT: Salzwedel, Karl
 APPLICANT: Li, Feng
 APPLICANT: Wild, Carl T.
 APPLICANT: Allaway, Graham P.
 APPLICANT: Freed, Eric O.
 TITLE OF INVENTION: Inhibition of HIV-1 Replication by Distribution of the Processing
 of the Viral Capsid-Spacer Peptide 1 Protein
 FILE REFERENCE: 1900_0430003
 CURRENT APPLICATION NUMBER: US/10/851,637
 CURRENT FILING DATE: 2004-05-24
 PRIOR APPLICATION NUMBER: US 10/766,528
 PRIOR FILING DATE: 2004-01-29
 PRIOR APPLICATION NUMBER: US 60/496,660
 PRIOR FILING DATE: 2003-08-21
 PRIOR FILING DATE: 2004-01-29
 NUMBER OF SEQ ID NOS: 115
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO: 88
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Artificial Sequence
 FEATURE:
 OTHER INFORMATION: Mutant SP1 region in HIV-1 NL4-3
 US-10-851-637-88

Query Match 35.8%; Score 24; DB 17; Length 13;
 Best Local Similarity 50.0%; Pred. No. 1.5e+03;
 Matches 4; Conservative 3; Mismatches 1; Indels 0; Gaps 0;

Qy 4 QVSPYTL 11
 Db 6 QVNPATIM 13

RESULT 8
 US-10-226-007-782
 Sequence 782, Application US/10226007
 Publication No. US20030105277A1
 GENERAL INFORMATION:
 APPLICANT: Myriad Genetics, Inc.
 APPLICANT: Morham, Scott
 APPLICANT: Hobden, Adrian
 APPLICANT: Zavitz, Kenton
 TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
 FILE REFERENCE: 5005_01
 CURRENT APPLICATION NUMBER: US/10/226,007
 CURRENT FILING DATE: 2002-11-15
 PRIOR APPLICATION NUMBER: US 60/313,883
 PRIOR FILING DATE: 2001-08-21
 NUMBER OF SEQ ID NOS: 1673
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 782
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Human herpesvirus 4
 US-10-226-007-782

Query Match 34.3%; Score 23; DB 14; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NQEQVSPY 8
 Db 1 NEEPPPPY 8

RESULT 9
 US-10-226-007-794
 Sequence 794, Application US/10226007
 Publication No. US20030105277A1
 GENERAL INFORMATION:
 APPLICANT: Myriad Genetics, Inc.
 APPLICANT: Morham, Scott
 APPLICANT: Hobden, Adrian
 APPLICANT: Zavitz, Kenton
 TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
 FILE REFERENCE: 5005_01
 CURRENT APPLICATION NUMBER: US/10/226,007
 CURRENT FILING DATE: 2002-11-15
 PRIOR APPLICATION NUMBER: US 60/313,883
 PRIOR FILING DATE: 2001-08-21
 NUMBER OF SEQ ID NOS: 1673
 SOFTWARE: PatentIn version 3.1
 SEQ ID NO: 794
 LENGTH: 13
 TYPE: PRT
 ORGANISM: Human herpesvirus 4
 US-10-226-007-794

Query Match 34.3%; Score 23; DB 14; Length 13;
 Best Local Similarity 50.0%; Pred. No. 2.2e+03;
 Matches 4; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

Qy 1 NQEQVSPY 8
 Db 2 NEEPPPPY 9

RESULT 10
 US-10-226-007-805
 Sequence 805, Application US/10226007
 Publication No. US20030105277A1

GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005_01
; SEQ ID NO: 805
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 805
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-805

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NOEQVSPY 8
Db 3 NEEPPPPY 10

RESULT 11
US-10-226-007-815
; Sequence 815, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005_01
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 815
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-815

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NOEQVSPY 8
Db 4 NEEPPPPY 11

RESULT 12
US-10-226-007-824
; Sequence 824, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Morham, Scott
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; APPLICANT: Myriad Genetics, Inc.
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005_01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-412-897-20

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NOEQVSPY 8
Db 5 NEEPPPPY 12

RESULT 13
US-10-226-007-832
; Sequence 832, Application US/10226007
; Publication No. US20030105277A1
; GENERAL INFORMATION:
; APPLICANT: Myriad Genetics, Inc.
; APPLICANT: Zavitz, Kenton
; APPLICANT: Hobden, Adrian
; TITLE OF INVENTION: Compositions and Therapeutic Methods for Viral Infection
; FILE REFERENCE: 5005_01
; CURRENT APPLICATION NUMBER: US/10/226,007
; CURRENT FILING DATE: 2002-11-15
; PRIOR APPLICATION NUMBER: US 60/313,883
; PRIOR FILING DATE: 2001-08-21
; NUMBER OF SEQ ID NOS: 1673
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO: 832
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Human herpesvirus 4
; US-10-226-007-832

Query Match 34.3%; Score 23; DB 14; Length 13;
Best Local Similarity 50.0%; Pred. No. 2.2e+03; Indels 0; Gaps 0;
Matches 4; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
Qy 1 NOEQVSPY 8
Db 6 NEEPPPPY 13

RESULT 14
US-10-412-897-20
; Sequence 20, Application US/10412897
; Publication No. US2003022024A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES ENCODING THE HUMAN CITRON KINASE
; FILE REFERENCE: D0193 NP
; CURRENT APPLICATION NUMBER: US/10/412,897
; CURRENT FILING DATE: 2003-04-11
; PRIOR APPLICATION NUMBER: D0193 NP
; PRIOR FILING DATE: 2002-04-12
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO: 20
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-412-897-20

Query Match 34.3%; Score 23; DB 15; Length 13;

```
Best Local Similarity 100.0%; Pred. No. 2.2e+03;
Matches 5; Conservative 0; Mismatches 0; Indels 0;
Gaps 0;
Qy      2  QEQVS 6
Db      2  QEQVS 6
```

```
RESULT 15
US-09-338-723a-7
; Sequence 7, Application US/09338723A
; Patent No. US2002001938A1
; GENERAL INFORMATION:
; APPLICANT: Huaming, Wang
; TITLE OF INVENTION: Phenol Oxidizing Enzymes
; FILE REFERENCE: GC561-2
; CURRENT APPLICATION NUMBER: US/09/338,723A
; CURRENT FILING DATE: 1999-06-23
; PRIOR APPLICATION NUMBER: 09/220,871
; PRIOR FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 11
; SEQ ID NO 7
; SOFTWARE: FASTSEQ for Windows Version 3.0
; LENGTH: 13
; TYPE: PRT
; ORGANISM: Stachybotrys chartarum
US-09-338-723a-7
```

```
Query Match 32.8%; Score 22; DB 9; Length 13;
Best Local Similarity 80.0%; Pred. No. 3.5e+03;
Matches 4; Conservative 0; Mismatches 1; Indels 0;
Gaps 0;
Qy      4  QVSPY 8
Db      3  QVMPY 7
```

Search completed: April 12, 2005, 11:04:24
 Job time : 130 secs

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OM protein - protein search, using sw model

Run on: April 12, 2005, 10:46:01 ; Search time 42 Seconds

(without alignments)
29.781 Million cell updates/sec

Title: US-09-674-616A-2

Perfect score: 67

Sequence: 1 NQEQQVSPVLLKG 13

Scoring table: BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 246

Minimum DB seq length: 13
Maximum DB seq length: 13

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR 79;*
1: _pir1;*
2: _pir2;*
3: _pir3;*
4: _pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	20	29.9	13	2 S47361	T-cell antigen rec
2	20	29.9	13	2 B56864	dipeptidyl-peptidase IV (EC 3.4.14.5) - bovine (fragment)
3	19	28.4	13	2 PI0157	Ig kappa chain V-I
4	19	28.4	13	2 S32473	lymnaDFamide 3 - 9
5	18	26.9	13	2 A61458	Ig kappa chain V-I
6	18	26.9	13	2 A61458	Ig kappa chain V-I
7	17	25.4	13	1 UNBO	neurotoxin - bovi extracellular lipa
8	17	25.4	13	2 A4818	neurotoxin [valid
9	17	25.4	13	2 A28505	neurotoxin - comm
10	17	25.4	13	2 A61067	neurotoxin - quin
11	17	25.4	13	2 B33608	Ig heavy chain CRD
12	17	25.4	13	2 P0256	tryptophyllin-13 -
13	17	25.4	13	2 A05174	equitin toxin 1A - 8
14	16	23.9	13	2 PC1149	glutathione transf
15	16	23.9	13	2 A61514	actin 7 - soybean
16	15	22.4	13	2 S15755	microbial collagen
17	15	22.4	13	2 B26093	glandular kallikre
18	15	22.4	13	2 A54326	glutathione transf
19	15	22.4	13	2 B28810	T-cell antigen rec
20	15	22.4	13	2 S47358	Ig H chain V-D-J r
21	15	22.4	13	2 PH1599	alpha-peptide/alg
22	14	20.9	13	2 P00038	Ig kappa chain V-I
23	14	20.9	13	2 D61458	Ig kappa chain V-I
24	14	20.9	13	2 B61458	T-cell antigen rec
25	14	20.9	13	2 S47362	T-cell antigen rec
26	14	20.9	13	2 S47380	conceptus protein
27	14	20.9	13	2 B61233	Ig H chain V-D-J r
28	14	20.9	13	2 PH1595	T-cell receptor al
29	14	20.9	13	2 PH0786	

ALIGNMENTS

RESULT 1

S47361

T-cell antigen receptor VJ junction beta chain - human

C;Species: Homo sapiens (man)

C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 05-Nov-1999

C;Accession: S47361

R;Lehner, P.J.

submitted to the EMBL Data Library, August 1994

A;Description: Human HLA-A0201 restricted recognition of influenza A is dominated by T cell

A;Accession: S47355

A;Status: Preliminary

A;Molecule type: mRNA

A;Residues: 1-13 <LEH>

A;Cross-references: EMBL:Z35685; NID:9527459; PIDN:CAA84754.1; PID:9527460

C;Keywords: T-cell receptor

Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;Query Match 29.9%; Score 20; DB 2; Length 13;
Best Local Similarity 80.0%; Pred. No. 1.6e+03; Mismatches 0; Indels 0; Gaps 0;

RESULT 3

PL057 Ig kappa chain V-II region (anti-myelin-associated glycoprotein, PBC) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 07-Feb-1997

C;Accession: PR01577; C61458

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

A;Title: Expression of a public idiotypic by human monoclonal IgM directed to myelin-associated protein

A;Reference number: A61458; MUID:90039128; PMID:2478851

A;Molecule type: protein

A;Residues: 1-13 <BRO>

A;Status: preliminary

A;Cross-references: 1-13 <BR2>

C;Comment: This protein is one of monoclonal IgM reactive with myelin-associated glycoprotein

C;Keywords: glycoprotein; heterotetramer; immunoglobulin

Query Match 28.4%; Score 19; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 2.5e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 6 SPYTL 10
Db 7 SPVTL 11

RESULT 4

S32473 LymanDramide 3 - great pond snail

C;Species: Lymanea stagnalis (great pond snail)

C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 09-Jul-2004

C;Accession: S32473

R;Johansen, A.H.; Rehfeld, J.F.

Bur. J. Biochem. 213: 875-879. 1993

A;Title: LymanDramides, a new family of neuropeptides from the pond snail, Lymanea stagnalis

A;Reference number: S32471; MUID:9338777; PMID:8477756

A;Accession: S32473

A;Molecule type: protein

A;Residues: 1-13 <JOH>

A;Cross-references: UNIPROT:P80180; PIDN:AAB26364.1; PMID:g299831

C;Keywords: amidated carboxyl end; neuropeptide

F;1/3/Modified site: amidated carboxyl end (Phe) #status predicted

Query Match 28.4%; Score 19; DB 2; Length 13;

Best Local Similarity 42.9%; Pred. No. 2.5e+03; Indels 0; Gaps 0;

Matches 3; Conservative 1; Mismatches 3; Indels 1; Gaps 0;

Qy 7 PTLLKG 13
Db 1 PDRISG 7

RESULT 5

B61458 Ig kappa chain V-II region (BLA) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996

C;Accession: B61458

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotypic by human monoclonal IgM directed to myelin-associated protein

A;Reference number: A61458; MUID:90039128; PMID:2478651

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <BRO>

C;Keywords: heterotetramer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 3.9e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 6 SPYTL 10
Db 7 SPVTL 11

RESULT 6

Ig kappa chain V-II region (BOU) - human (fragment)

C;Species: Homo sapiens (man)

C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 16-Aug-1996

C;Accession: A61458; PL0156

R;Brouet, J.C.; Dellagi, K.; Gendron, M.C.; Chevalier, A.; Schmitt, C.; Mihaesco, E.

J. Exp. Med. 170, 1551-1558, 1989

A;Title: Expression of a public idiotypic by human monoclonal IgM directed to myelin-associated protein

A;Reference number: A61458; PMID:2478651

A;Molecule type: protein

A;Residues: 1-13 <BRO>

C;Comment: This protein is one of monoclonal IgM reactive with myeloma-associated glycoprotein

C;Keywords: heterotetramer; immunoglobulin

Query Match 26.9%; Score 18; DB 2; Length 13;

Best Local Similarity 80.0%; Pred. No. 3.9e+03; Indels 0; Gaps 0;

Matches 4; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 6 SPYTL 10
Db 7 SPVTL 11

RESULT 7

UNBO neurotensin - bovine

C;Species: Bos primigenius taurus (cattle)

C;Date: 18-Dec-1981 #sequence_revision 18-Dec-1981 #text_change 24-Feb-1995

C;Accession: A01420

R;Carraway, R.; Leeman, S.E.

J. Biol. Chem. 250, 1907-1911, 1975

A;Title: The amino acid sequence of a hypothalamic peptide, neurotensin.

A;Reference number: A92172; MUID:75095678; PMID:1167549

A;Accession: A01420

A;Molecule type: protein

A;Residues: 1-13 <CAR>

A;Experimental source: hypothalamus

R;Carraway, R.; Leeman, S.E.

J. Biol. Chem. 250, 1912-1918, 1975

A;Title: The synthesis of neurotensin.

A;Reference number: A92173; MUID:75095679; PMID:1112838

A;Content: annotation; synthesis

C;Superfamily: neuropeptide; pyroglutamic acid

C;Keywords: neuropeptide; pyroglutamic acid (Gln) #status experimental

F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 1; Length 13;

Best Local Similarity 75.0%; Pred. No. 6e+03; Indels 0; Gaps 0;

Matches 3; Conservative 0; Mismatches 1; Indels 1; Gaps 0;

Qy 7 PYTL 10
Db 10 PYL 13

RESULT 8

A44818 A44818 extracellular lipase - Pseudomonas aeruginosa (fragment)

C;Species: Pseudomonas aeruginosa

C;Date: 31-Mar-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004

C;Accession: A44818

R;Gilbert, E.J.; Cornish, A.; Jones, C.W.

Query Match 26.9%; Score 18; DB 2; Length 13;

J. Gen. Microbiol. 137, 2223-2229, 1991
 A;Title: Purification and properties of extracellular lipase from *Pseudomonas aeruginosa*
 A;Reference number: A44818 ; MUID:92085040; PMID:1748875
 A;Status: preliminary; not compared with conceptual translation
 A;Molecule type: nucleic acid
 A;Cross-references: UNIPROT:Q9L6C7; UNIPROT:P95419
 A;Experimental source: strain TE3125
 C;Superfamily: *Pseudomonas* triacylglycerol lipase

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 6e+03;
 Matches 4; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 6 SPYTLK 12
 Db 1 STYQTQTK 7

RESULT 9
 A28505
 neurotensin [validated] - chicken
 C;Species: *Gallus gallus* (chicken)
 C;Date: 19-Nov-1988 #sequence_revision 18-Aug-2000 #text_change 09-Jul-2004
 C;Accession: A28505
 R;Iwabuchi, H.; Komori, S.; Ohashi, H.; Kimura, S.
 Jpn. J. Pharmacol. 44, 455-459, 1987
 A;Title: The amino acid sequence of a smooth muscle-contracting peptide from chicken rectum
 A;Reference number: A28505 ; MUID:88063566; PMID:36824499
 A;Accession: A28505
 A;Molecule type: protein
 A;Residues: 1-13 <IWA>
 A;Cross-references: UNIPROT:P13724
 A;Experimental source: rectum
 C;Comment: The peptide isolated from rectum is identical with chicken neurotensin and has the same biological activity
 C;Superfamily: neurotensin
 C;Keywords: hormone, neuropeptide; pyroglutamic acid
 F;1-13/Product: neurotensin #status experimental <NTM>
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
 Db 10 PYTL 13

RESULT 10
 A61067
 neurotensin - common frog
 C;Species: *Rana temporaria* (common frog)
 C;Accession: A61067
 R;Shaw, C.; McKay, D.M.; Halton, D.W.; Thim, L.; Buchanan, K.D.
 Regul. Pept. 38, 23-31, 1992
 A;Title: Isolation and primary structure of an amphibian neurotensin.
 A;Reference number: A61067 ; MUID:92245104; PMID:15746601
 A;Accession: A61067
 A;Molecule type: protein
 A;Residues: 1-13 <SHA>
 A;Cross-references: UNIPROT:P41536
 A;Note: this peptide was identified in brain, intestine, and rectum, but not in stomach
 C;Keywords: brain; intestine; neuropeptide; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
 Db 10 PYTL 13

RESULT 11
 A53608
 neurotensin - guinea pig
 C;Species: *Cavia porcellus* (guinea pig)
 C;Date: 07-Oct-1994 #sequence_revision 07-Oct-1994 #text_change 09-Jul-2004
 C;Accession: A53608
 R;Shaw, C.; Thim, L.; Conlon, J.M.
 FEBS Lett. 202, 187-191, 1986
 A;Title: [Ser(7)]neurotensin: isolation from guinea pig intestine.
 A;Reference number: A53608 ; MUID:86248085; PMID:3087775
 A;Accession: A53608
 A;Status: preliminary
 A;Molecule type: protein
 A;Residues: 1-13 <SHA>
 A;Cross-references: UNIPROT:P32560
 C;Keywords: neurotensin; pyroglutamic acid
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 75.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 7 PYTL 10
 Db 10 PYTL 13

RESULT 12
 PT0256
 Ig heavy chain CRD3 region (clone 2-115C) - human (fragment)
 C;Species: *Homo sapiens* (man)
 C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Aug-1996
 C;Accession: PT0256
 R;Yamada, M.; Wasserman, R.; Reichard, B.A.; Shane, S.; Caton, A.J.; Rovera, G.
 J. Exp. Med. 173, 395-407, 1991
 A;Title: Preferential utilization of specific immunoglobulin heavy chain diversity and j₅ gene usage
 A;Reference number: PT0222; MUID:9108337; PMID:1899102
 A;Accession: PT0256
 A;Molecule type: DNA
 A;Residues: 1-13 <YAM>
 A;Experimental source: B lymphocyte
 C;Keywords: heterotetramer; immunoglobulin

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 6e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 YTLLKG 13
 Db 4 YDMLTG 9

RESULT 13
 A05174
 tryptophyllin-13 - Rohde's leaf frog
 C;Species: *Phyllomedusa rohdei* (Rohde's leaf frog)
 C;Accession: A05174
 R;Montecucchi, P.C.; Gozzini, L.; Esgaamer, V.
 Int. J. Pept. Protein Res. 27, 175-182, 1986
 A;Reference number: A05174
 A;Accession: A05174
 A;Molecule type: protein
 A;Residues: 1-13 <MON>
 A;Cross-references: UNIPROT:P04096
 C;Superfamily: unassigned animal peptides

C;Keywords: Pyroglutamic acid; Skin
 F;1/Modified site: pyrrolidone carboxylic acid (Gln) #status experimental

Query Match 25.4%; Score 17; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 6e+03;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 4 QVSPY 8
 Db 1 QEKPY 5

RESULT 14

PC1149 equinatoxin 1A - sea anemone (Actinia equina) (fragment)

C;Species: Actinia equina.

C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 07-May-1999

C;Accession: PC1149

R;Komatsu, S.; Furukawa, K.; Abe, K.; Hirano, H.; Ueda, M.
 Chem. Pharm. Bull. 40, 2873-2875; 1992

A;Title: Isolation and characterization of equinatoxins from the sea anemone *Actinia equina*

A;Reference number: PC1149; MUID:93099631; PMID:1361161

A;Accession: PC1149

A;Molecule type: protein

A;Residues: 1-13 <ROM>

C;Keywords: toxin

Query Match 23.9%; Score 16; DB 2; Length 13;
 Best Local Similarity 60.0%; Pred. No. 9.3e+03;
 Matches 3; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

Qy 1 NQEY 5
 Db 4 NQAEV 8

RESULT 15

A61514 Glutathione transferase (EC 2.5.1.18), 26k - fluke (*Schistosoma japonicum*) (fragment)

C;Species: *Schistosoma japonicum*

C;Date: 15-Oct-1994 #sequence_revision 15-Oct-1994 #text_change 09-Jul-2004

C;Accession: A61514

R;Mitchell, G.F.

Mol. Biochem. Parasitol. 27, 249-256, 1988

A;Title: Expression of an enzymatically active parasite molecule in *Escherichia coli*: So

A;Reference number: A61514; MUID:88142994; PMID:3278228

A;Accession: A61514

A;Status: preliminary

A;Molecule type: protein

A;Residues: 1-13 <MTT>

A;Cross-references: UNIPROT:P08515

C;Keywords: transferase

Query Match 23.9%; Score 16; DB 2; Length 13;
 Best Local Similarity 50.0%; Pred. No. 9.3e+03;
 Matches 3; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

Qy 8 YTLLKG 13
 Db 6 YWKIKG 11

Search completed: April 12, 2005, 10:50:32
 Job time : 43 secs

CC -!- CATALYTIC ACTIVITY: Isocitrate + NAD(+) = 2-oxoglutarate + CO(2) + NADH
 CC -!- SUBUNIT: Heterooligomer of subunits alpha, beta, and gamma in the apparent ratio of 2:1:1 (By similarity).
 CC -!- SUBCELLULAR LOCATION: Mitochondrial.
 CC -!- SIMILARITY: Belongs to the isocitrate and isopropylmalate dehydrogenases family.
 CC HSC-2DPAGE; Ps4836; DOG;
 DR InterPro; IPR01800; I80dh;
 DR PROSITE; PS00470; IDH_IMDH; PARTIAL.
 KW Direct protein sequencing; Mitochondrion; NAD; Oxidoreductase;
 KW Tricarboxylic acid cycle.
 FT NON TER 13 13 MW: 1356 MW;
 SQ SEQUENCE 13 AA; 1356 MW; 9ABFFBC2B2A34B2D1 CRC64;

Query Match 29.9%; Score 20; DB 1; Length 13;
 Best Local Similarity 40.0%; Pred. No. 9.2e+03;
 Matches 4; Conservative 2; Mismatches 4; Indels 0; Gaps 0;

Qy 4 VSPYTLKLKG 13
 Db 3 EVQTVTLIPG 12

RESULT 3
 ID Q6T675 PRELIMINARY;
 AC Q6T675;
 DT 05-JUL-2004 (TREMBrel. 27, Created)
 DT 05-JUL-2004 (TREMBrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBrel. 27, Last annotation update)
 DE MHC class Ib antigen (Fragment).
 GN Name-PaaN-AG;
 OS Papio anubis.
 OC Mammalia; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
 OC Cercopithecinae; Papio.
 OX NCBI_TaxID:211508;
 RN SEQUENCE FROM N.A.
 RC TISSUE=Term placenta;
 RA Langat D.K., Morales P.J., Fazoleabas A.T., Hunt J.S.;
 RL Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY34094; ARR12067.1; -.
 FT NON TER 13 13 MW: 1456 MW;
 SQ SEQUENCE 13 AA; 1456 MW; 3768BCBF608B417 CRC64;

Query Match 29.9%; Score 20; DB 2; Length 13;
 Best Local Similarity 57.1%; Pred. No. 9.2e+03;
 Matches 4; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 5 VSPYTLI 11
 Db 4 MAPRTLL 10

RESULT 4
 CHEP_PARID_CHEP_PARID STANDARD; PRT; 13 AA.
 AC P42718;
 DT 01-NOV-1 1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Chymotryptic Peptide.
 OS Parapolybia indica.
 OS Parapolybia indica; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Hymenoptera; Aculeata; Vespoidea; Vespidae; Polistinae; Parapolybia.
 OX NCBI_TaxID:31921;

RN SEQUENCE FROM N.A.
 TISSUE=Tracheobronchial mucosa;
 RA Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M., Zouina-Galigue S., Pigny P., Degand P., Aubert J., Porchet N.;
 RC TISSUE=Venom;
 RA Toki T., Yasuhara T., Nakajima T.;

RT "Isolation and sequential analysis of peptides on the venom sac of Parapolybia indica.";
 RT Eisei Dobutsu 33:105-111(1988).
 KW Amidation; Chemotaxis; Direct protein sequencing.
 MOD RES 13 13 AA; 1298 MW;
 SQ Sequence 13 AA; 5C950CB8E39D5873 CRC64;
 Query Match 28.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 100.0%; Pred. No. 1.4e+44;
 Matches 4; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 10 LLIKKG 13
 Db 4 LLIKKG 7

RESULT 5
 NP3_LYNST STANDARD; PRT; 13 AA.
 ID NP3_LYNST
 AC P80180;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE Lymania-Di-amide 3.
 OS Lymania stigmalis (Great pond snail).
 OC Eukaryota; Metazoa; Mollusca; Gastropoda; Pulmonata; Basommatophora; Lymaneoidea; Lymaneidae; Lymanea.
 OC NCBI_TaxID=6523;
 RN [1]
 RP
 RC TISSUE=ganglion; PubMed=8477756;
 RX MEDLINE=93238777;
 RA Johnsen A.H., Rehfeld J.F.;
 RT Lymania stigmalis, a new family of neuropeptides from the pond snail, invertebrates?; RT
 RL Eur. J. Biochem. 213:875-879(1993).
 CC !- SUBCELLULAR LOCATION: Secreted.
 CC !- SIMILARITY: Related to the cholecystokinin (CCK) family.
 CC DR PIR; S32473; S32473.
 DR TISSUE=Term placenta; Direct protein sequencing; Neuropeptide.
 KW Phenylalanine amide.
 MOD RES 13 13
 FT UNSURE 12 12
 SQ SEQUENCE 13 AA; 1462 MW; 9CA07BA3F5D5B865 CRC64;
 Query Match 28.4%; Score 19; DB 1; Length 13;
 Best Local Similarity 42.9%; Pred. No. 1.1e+44;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 7 PYTTLKG 13
 Db 1 PYPRISG 7

RESULT 6
 Q14890 PRELIMINARY; PRT; 13 AA.
 ID Q14890
 AC Q14890;
 DT 01-NOV-1996 (TREMBrel. 01, Created)
 DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBrel. 19, Last annotation update)
 DB Mucin (Fragment).
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Tracheobronchial mucosa;
 RA Guyonnet-Duperat V., Audie J., Debailleul V., Laine A., Buisine M., Zouina-Galigue S., Pigny P., Degand P., Aubert J., Porchet N.;
 RA "Characterization of the human mucin gene MUC5AC: a consensus
 RT

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Hyloidea; Hylidae;
 OC Phylomedusinae; Phylomedusa;
 OX NCBI_TaxID=8394;
 RN [1]
 RP
 SEQUENCE.
 RA Montecuccchi P.C., Gozzini L., Erspamer V.;
 RT "Primary structure determination of a tryptophan-containing
 tridecapeptide from Phylomedusa rohdei."
 RL Int. J. Pept. Protein Res. 27:175-182 (1986).
 RT -1- SUBCELLULAR LOCATION: Secreted.
 CC -1- TISSUE SPECIFICITY: Skin.
 DR PIR; A05174; A05174.
 KW Amphibian defense peptide; Direct protein sequencing;
 KW Pyrrolidone carboxylic acid.
 FT MOD_RES 1 Pyrrolidone carboxylic acid.
 SQ SEQUENCE 13 AA; 1646 MW; 33BF33A21222773 CR064;
 SEQUENCE 13 AA; 1646 MW; 33BF33A21222773 CR064;
 Query Match Score 17; DB 1; Length 13;
 Best Local Similarity 60.0%; Pred. No. 3.5e+04;
 Matches 3; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
 Qy 4 QVSPY 8
 Db 1 |
 1 QEKPY 5

RESULT 15
 Q6S4RS ID Q6S4RS PRELIMINARY; PRT; 13 AA.
 AC Q6S4RS;
 DT 05-JUL-2004 (T-EMBLrel. 27, Created)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)
 DE Alpha tubulin (Fragment).
 OS Leishmania hagasi.
 OC
 OX NCBI_TaxID=4271;
 RN [1]
 RP
 SEQUENCE FROM N.A.
 STRAIN=MHOM/BR/00/1669;
 RA Purdy J.E.; Wilson M.E.;
 RL Submitted to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY466450; AAR8132.1; -.
 FT NON_TER 1
 SQ SEQUENCE 13 AA; 1488 MW; 3F361B068941B18 CR064;
 Query Match Score 17; DB 2; Length 13;
 Best Local Similarity 42.9%; Pred. No. 3.5e+04;
 Matches 3; Conservative 1; Mismatches 3; Indels 0; Gaps 0;
 Qy 2 QEKVSPY 8
 Db 7 : |
 7 EEDVEEY 13

Search completed: April 12, 2005, 10:53:34
 Job time : 176 secs

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